SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Tobin, James

   (ii) TITLE OF INVENTION: HUMAN INTERLUEKIN-11 RECEPTOR

   (iii) NUMBER OF SEQUENCES: 4

   (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: Genetics Institute, Inc.
       (B) STREET: 87 CambridgePark Drive
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       (F) ZIP: 02140

   (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: Floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

   (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER:
       (B) FILING DATE:
       (C) CLASSIFICATION:

   (viii) ATTORNEY/AGENT INFORMATION:
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       (C) REFERENCE/DOCKET NUMBER: GI5252

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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2456 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 734..1999

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TCGCCCACCC CCAGCCTCTG GCAGCAGCCA GGGCATCTGG ATCTGCTTAA CTACACAGCC      60

CCAGCCTGCA CCCTAGCCCC ATCCAGCTTC ACAAACTGGA GACCAACGAA GTGTCAAGAG     120

CCAGGCCCAG CTGAGTGGCC CAAGTAGCCA GACCAAGGAG CCAGGTTCAG GCGAGAAGCC     180

TGGCAGCCAG GGCAGGGGTG GGCCTCAGGG TGGGAGTGCA GGATGGGCTC AGATCCATGA     240

TGACACCCTT CCCCCAGGGT GATAAGGTCT GCCTAGGTTA ATCAGAGGCA GTGATAAGCC     300

CTGGACCAGG TGGGGGTAAA TACCAGAATT CCCAACAGCT GGACTGGAGG GGTTAATGGG     360

AGTGGCTGAG CTGGTGCCAG TGCTTGGTGC CAGGGGTGGG CGCCAAGGGC AGTGGAGGGG     420

GAGTTGCTGG CACAGTCTGT TGCCTCCGGC TTTTGTTCTG GGCCCTAAGC CCAGGACTGA     480

GATGGAGGGT GTGAGGGGGT GTGTGTGTCC GTGTGTGTGT GTGTGTGTGT GTGCGCGCGC     540

ACGCACATGC AAAGCACTGG GTATACAGTG GGAAAGGGGA CCTCAGGTCA GTTCCCGCAG     600
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TGATTTCTAA CAGCCTTACC CCACTTGGTG CATCAATTTT TCTCCTAGGA AGCCTCAGTT          660

TTGGAGAGGA AGAGCCAGGC TTTAGCCTCC CATCTCAGGG GTCGGGGATT TTTGACTCTA          720

CCTCTCCCCA CAG ATG AGC AGC AGC TGC TCA GGG CTG GGG AGC AGG GTC CTG          769
               Met Ser Ser Ser Cys Ser Gly Leu Gly Ser Arg Val Leu
               1                       5                       10

GTG GCC GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG             817
Val Ala Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln
         15                  20                  25

GCC TGG GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG             865
Ala Trp Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val
         30                  35                  40

AAG CTG TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT                 913
Lys Leu Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe
     45                  50                  55                  60

CGG GAT GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG             961
Arg Asp Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly
     65                  70                  75

CAT GAA CTG GTC CTG GCC CAG GCA AGC GAC AGC ACT GAT GAG GGC ACC TAC        1009
His Glu Leu Val Leu Ala Gln Ala Ser Asp Ser Thr Asp Glu Gly Thr Tyr
     80                  85                  90

ATC TGC CAG ACC CTG GAT GGT GCA CTT CTT GGG GGC GGC ACA GTG ACC CTG CAG    1057
Ile Cys Gln Thr Leu Asp Gly Ala Leu Leu Gly Gly Gly Thr Val Thr Leu Gln
     95                  100                 105

CTG GGC TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC            1105
Leu Gly Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp
     110                 115                 120

TAT GAG AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA           1153
Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu
     125                 130                 135                 140
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```
CCC ACC CGC TAC CTC ACC TCC AGG AAG ACA GTC CTA GGA GCT        1201
Pro Thr Arg Tyr Leu Thr Ser Arg Lys Thr Val Leu Gly Ala
            145                 150                 155

GAT AGC CAG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CAG        1249
Asp Ser Gln Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Gln
            160                 165                 170

GAT CCC CTA GGG GCT GCC CGC TGT GTC CAC GGG GCT GAG TGG        1297
Asp Pro Leu Gly Ala Ala Arg Cys Val His Gly Ala Glu Trp
            175                 180                 185

AGC CAG TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA GGT GCC AGC    1345
Ser Gln Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Gly Ala Ser
            190                 195                 200

ACA CGC CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA    1393
Thr Arg Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro
            205                 215                 220

CCC CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA CTG    1441
Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Leu
            225                 230                 235

CGA GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC   1489
Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe
            240                 245                 250

CTG CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG   1537
Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp
            255                 260                 265

TCC ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG   1585
Ser Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val
            270                 275                 280

GCT GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT   1633
Ala Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp
            285         290         295                 300
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FIGURE 5 (CONT'D)

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GCT GGC ACC TGG AGC ACC TGG GAG CCG GGA ACT CCG AGC        1681
Ala Gly Thr Trp Ser Thr Trp Glu Pro Gly Thr Pro Ser
            305                 310                 315

ACT GGG ACC ATA CCA AAG GAG ATA CCA TGG GGC CAG CTA CAC ACG    1729
Thr Gly Thr Ile Pro Lys Glu Ile Pro Trp Gly Gln Leu His Thr
            320                 325                 330

CAG CCA GAG GAG GTG CCT CAG GTG GAC AGC CCT CCT CCA AGG CCC    1777
Gln Pro Glu Glu Val Pro Gln Val Asp Ser Pro Pro Pro Arg Pro
            335                 340                 345

TCC CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG    1825
Ser Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu
            350                 355                 360

CAG GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG    1873
Gln Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu
            365                 370                 375             380

GTG GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGA CGG GGT        1921
Val Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Arg Gly
            385                 390                 395

GGG AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA    1969
Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro
            400                 405                 410

GTG GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT    2019
Val Asp Arg Arg Pro Gly Ala Pro Asn Leu
            415                 420

CGGCAGATTC CACCTATAAT TCTGTCTTGC TGGTGTGGAT GGATGGACAG ATAGAAACCA   2079

GGCAGGACAG TAGATCCCTA TGGTTGGATC TCAGCTGGAA GTTCTGTTTG GAGCCCATTT   2139

CTGTGAGACC CTGTATTTCA AATTTGCAGC TGAAAGGTGC TTGTACCTCT GATTTCACCC   2199

CAGAGTTGGA GTTCTGCTCA AGGAACGTGT GTAATGTGTA CATCTGTGTC CATGTGTGAC   2259
```

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CATGTGTCTG TGAGGCAGGG AACATGTATT CTCTGCATGC ATGTATGTAG GTGCCTGGGG   2319

AGTGTGTGTG GGTCCTTGGC TCTTGGCCTT TCCCCTTGCA GGGGTTGTGC AGGTGTGAAT   2379

AAAGAGAATA AGGAGTTCT TGGAGATTAT ACTCAGAAAA AAAAAAAAAA AGTCGACGCG   2439

GCCGCGAATT CCTGCAG   2456

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 422 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala
1   5   10   15

Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
            20   25   30

Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Cys Cys
35   40   45

Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu
            50   55   60

Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val
65   70   75   80

Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys Gln Thr
                    85   90   95

Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro
                    100   105   110

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Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe
115   120   125

Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr
130   135   140

Leu Thr Ser Tyr Arg Lys Thr Val Leu Gly Ala Asp Ser Gln Arg
145   150   155   160

Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly
165   170   175

Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg
180   185   190

Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Arg Leu Leu
195   200   205

Asp Val Glu Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Gln Gly Leu
210   215   220

Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg Ala Ser Trp
225   230   235   240

Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys Phe
245   250   255

Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
260   265   270

Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
275   280   285

His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
290   295   300

Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr Ile
305   310   315   320

Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu Val

```
                325                     330                     335
Glu Pro Gln Val Asp Ser Pro Ala Pro Arg Pro Ser Leu Gln Pro
                340                     345                     350

His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln Val Ala Val
                355                     360                     365

Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly Ala
                370                     375                     380

Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly Lys Asp Gly
385                     390                     395                     400

Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg Arg
                405                     410                     415

Pro Gly Ala Pro Asn Leu
                420
```

(2) INFORMATION FOR SEQ ID NO:3:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1714 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (iii) HYPOTHETICAL: NO

   (ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 34..1359

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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```
TTCTTAGCCT GATAGGAGGA AGTCTTGGAG GCC ATG GCA CTC AGT CAC TGT GAT       54
                                      Met Ala Leu Ser His Cys Asp
                                       1                   5

TAT CAA GAT GAG CAG CAG CTG CTC AGG GCT GAC CAG GGT CCT GGT GGC       102
Tyr Gln Asp Glu Gln Gln Leu Leu Arg Ala Asp Gln Gly Pro Gly Gly
         10              15              20

CGT GCT ACA GCC CTG GTG TCT TCC TCC CCC TGC CCC CAA GCT TGG           150
Arg Ala Thr Ala Leu Val Ser Ser Ser Pro Cys Pro Gln Ala Trp
             25              30              35

GGT CCT CCA GGG GTC CAG TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG       198
Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu
         40              45              50              55

TGC TGC CCC GGA GTG AGT GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT       246
Cys Cys Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp
     60              65              70

GGA GAT TCA AGG CTG CTC CAG GGA CCT GGG TCT GAC GGC TTA CAC AGA       294
Gly Asp Ser Arg Leu Leu Gln Gly Pro Gly Ser Asp Gly Leu His Arg
         75              80              85

CTG GTC TTG GCC CAG GTG GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC       342
Leu Val Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys
         90              95             100

CAG ACC CTG GAT GGT GTA TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC       390
Gln Thr Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly
        105             110             115

TTT CCC CCA GCA CGT CCT GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA       438
Phe Pro Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu
        120             125             130             135

AAC TTC TCC TGT ACT TGG AGT CCA GGC CAG GTC CAG AGC GGT TTG CCC ACC   486
Asn Phe Ser Cys Thr Trp Ser Pro Gly Gln Val Gln Ser Gly Leu Pro Thr
        140             145             150
```

```
CGC TAC CTT ACT TCC TAC AGG AAG ACG CTG CCA GGA GCT GAG AGT        534
Arg Tyr Leu Thr Ser Tyr Arg Lys Thr Leu Pro Gly Ala Glu Ser
                155             160             165

CAG AGG GAA AGT CCA TCC ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT    582
Gln Arg Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro
                    170             175             180

CTG GAG GCC TCC CGA TGT GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG    630
Leu Glu Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu
            185             190             195

TAC CGG ATC AAT GTG ACC GAG GTG AAC CCA CTG GGT GCC AGC ACG TGC    678
Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys
        200             205             210             215

CTA CTG GAT GTG AGA TTA CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA    726
Leu Leu Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln
                    220             225             230

GGA CTG CGG GTG GTG GAA TCC GTA CCT TAC CCG GGT CGC CTG CAT GCC    774
Gly Leu Arg Val Val Glu Ser Val Pro Tyr Pro Gly Arg Leu His Ala
                    235             240             245

AGC TGG ACA TAC CCT GCC TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC    822
Ser Trp Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu
                250             255             260

AAG TTC CGG TTG CAA TAC CGA CCA CAG CAT CCA GCC TGG ACG TCC ACG    870
Lys Phe Arg Leu Gln Tyr Arg Pro Gln His Pro Ala Trp Thr Ser Thr
                265             270             275

GTG GAG CCC ATT GGC TTG GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG    918
Val Glu Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly
                280             285             290             295

CTG CCA CAC GCG GTA CGA GTC AGT GCC AGA GTC GAC TTT CTG GAT GCT GGC  966
Leu Pro His Ala Val Arg Val Ser Ala Arg Val Asp Phe Leu Asp Ala Gly
                    300             305             310
```

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FIGURE 6B-4 (continued)

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ACC TGG AGC GCC TGG CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT    1014
Thr Trp Ser Ala Trp Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly
                    315             320             325

CCC CTG CAG GAG ATA CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG    1062
Pro Leu Gln Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln
            330             335             340

CTA GAG GTA GCT CAG GAG GAC AGC GCT CCT GCA AGG CCT            1110
Leu Glu Val Ala Gln Glu Asp Ser Pro Ala Arg Pro
345             350             355

TCC TTG CAG CCG GAC CCA CTT GAT CAC AGG GAC CCC TTG GAG        1158
Ser Leu Gln Pro Asp Arg Pro Leu Asp His Arg Asp Pro Leu Glu
        360             365             370             375

CAA GTA GCT GTG TTA GCG TCT CTG GGA ATC TTC TGC CTT GGC CTG    1206
Gln Val Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu
                380             385             390

GCT GTT GGA GCT CTG GCA CTG GGG CTC TGG AGG CTG AGA CGG AGT    1254
Ala Val Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser
            395             400             405

GGG AAG GAT GGA CCG CAA AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG    1302
Gly Lys Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro
        410             415             420

GTG GAA AAG CTT CCA GGA ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC    1350
Val Glu Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn
        425             430             435

TTC AGC TGATTTCATC TGTAACCCGG TCAGACTTGG GGTGGTTAAA AGGACAGGCA    1406
Phe Ser
440

GAAAGAGGCG GGGCAGTGGA TCCCTGTGGA TGGAGGTCTC AGCTGAAAGT CTGAGCTCTT    1466

TTCTTTGACA CCTATACTCC AAACTTGCTG CCGGCTGAAG GCTGTCTGGA CTTCCGATGT    1526
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CCTGAGGTGG AAGTCCACCT GAGGAATGTG TACAGAAGTC TGTGTTCCTG TGATCGTGTG    1586

TGTATGTGAG ACAGGGAGCA AAAGTTCTCT GCATGTGTGT ACAGATGATT GGAGAGTGTG    1646

TGCGGTCTTG GGCTTGGCCC TTCTGGGAAG TGTGAAGAGT TGAAATAAAA GAGACGGAAG    1706

TTTTTGGA                                                             1714
```

(2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 441 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Ala Leu Ser His Cys Asp Tyr Gln Asp Glu Gln Gln Leu Leu Arg
  1               5                  10                  15

Ala Asp Gln Gly Pro Gly Gly Arg Ala Thr Ala Leu Val Ser Ser Ser
                 20                  25                  30

Ser Pro Cys Pro Gln Ala Trp Gly Pro Gly Val Gln Tyr Gly Gln
                 35                  40                  45

Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser Ala Gly Thr
             50                  55                  60

Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu Gln Gly Pro
 65                  70                  75                  80

Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val Asp Ser Pro
                 85                  90                  95

Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val Ser Gly Gly
                100                 105                 110
```

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Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro Glu Val Ser
115   120   125

Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Gly
130   135   140

Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys Lys
145   150   155   160

Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser Thr Gly Pro
165   170   175

Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys Val Val His
180   185   190

Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr Glu Val Asn
195   200   205

Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu Gln Ser Ile
210   215   220

Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly
225   230   235   240

Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala Ser Trp Arg
245   250   255

Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala
260   265   270

Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu Glu Glu Val
275   280   285

Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg Val Ser Ala
290   295   300

Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser Pro Glu Ala
305   310   315   320

Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile Pro Asp Trp

45

```
                 325             330             335
Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala Gln Glu Asp
                340             345             350
Ser Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro Arg Pro Leu
                355             360             365
Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala Ser Leu Gly
                370             375             380
Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Leu Ala Leu Ala Gly Leu
                385             390             395             400
Trp Leu Arg Leu Arg Ser Gly Lys Asp Gly Pro Gln Lys Pro Gly
                405             410             415
Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly Ile Pro Asn
                420             425             430
Leu Gln Arg Thr Pro Glu Asn Phe Ser
                435             440
```